

ORIGINAL ARTICLE OPEN ACCESS

Traits Profiling and Genotype Selection in Common Bean (*Phaseolus vulgaris* L.) in Ethiopia Using the GT and GYT Biplot Analyses

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Received: 25 February 2025 | **Revised:** 23 September 2025 | **Accepted:** 7 October 2025

Funding: This work was supported and funded by the Ethiopian Institute of Agricultural Research (EIAR).

Keywords: biofortification | disease resistance | grain yield | iron | multitrait selection | zinc

ABSTRACT

Phaseolus vulgaris, a crucial legume worldwide, is essential for human consumption and provides an abundant supply of proteins, micronutrients, antioxidants, and bioactive compounds. A common bean breeder faces considerable challenges due to inherent trade-offs when attempting to simultaneously improve grain yield, Fe/Zn concentrations, and disease resistance. In this study, 118 common bean genotypes, along with two standard check cultivars, were evaluated using a randomized complete block design with a row-column arrangement, with two replicates in two locations during the Meher season in 2019/20. In our study, GT and GYT analyses were used to dissect the associations between various traits and to select superior genotypes based on multiple traits. The highest grain yield t ha⁻¹ was obtained from genotypes G18, G63, and G81. The assessed genotypes showed Fe concentration ranging from 41.4 to 89.4 ppm, with a mean of 51.6 ppm, whereas Zn concentration ranged from 17.7 to 37.2 ppm, with a mean of 24.5 ppm. The GT biplot explained 43.8% of the total variation, identifying donor genotypes with high Fe/Zn concentrations and disease resistance, whereas the GYT biplot accounted for 80.4% of the variation and revealed 10 high-performing, balanced genotypes. Positive correlations were observed between yield and plant height, Fe and Zn concentrations, and days to flowering and maturity, indicating the potential for simultaneous improvement in yield, micronutrient density, and disease resistance. Overall, the integration of GT and GYT biplot analyses enabled the identification of promising candidate genotypes for direct release (G63, G100, G81, G80, and G18) and trait-specific donors for crossing, offering a practical strategy for the development of biofortified bean cultivars with high yield and disease resistance.

1 | Introduction

Common bean (*Phaseolus vulgaris* L.) is a vital global legume that is essential for human consumption, providing a bountiful

source of proteins, micronutrients, antioxidants, and bioactive compounds (Karavidas et al. 2022). It contributes significantly to dietary energy and protein intake, providing approximately 15% of total daily calories and 36% of total daily protein in certain

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regions of Africa and the Americas (Schmutz et al. 2014). The crude protein content of common bean seeds ranges from 17.39% to 23.54% (Neupane et al. 2024).

In Ethiopia, common bean is among the most important pulse crops in terms of both area and production (CSA 2021). According to FAOSTAT (2021), a total of 354,907 ha is cultivated with common bean, producing 612,552 tons. The majority of production occurs in Oromia (43%), Amhara (25%), and the Southern Nations, Nationalities, and Peoples' Region (29%) (Miruts 2022). The crop serves as both a source of protein for local consumption and an important export commodity (Yohannes et al. 2020). Despite its importance, production is constrained by suboptimal agronomic practices, poor soil fertility, limited varietal development, water stress, weeds, pests, and diseases (Mohammed and Feleke 2022). Consequently, national average productivity (<2 tons/ha) remains below the global average of 2.5–3.5 tons/ha (CSA 2020).

Traditional crop variety trials often focus on a single trait, typically grain yield, whereas breeding decisions should consider multiple traits simultaneously (Raza et al. 2019). While several studies have aimed to improve common bean yield, traits related to agronomic performance, nutritional quality, and disease resistance have received less attention (Celmeli and Sari 2018; Gholizadeh et al. 2023), with most studies focusing solely on grain yield (Burbano-Erazo et al. 2021; Castiano et al. 2023; de Melo et al. 2023; de Souza et al. 2023). Two major challenges in breeding are genotype $\times$ environment ($G \times E$) interactions and unfavorable correlations among traits (Yan and Fréreau-Reid 2018; Yan 2024).

To address these challenges, traditional approaches like tandem selection have been employed, where one trait is selected to an acceptable level before selecting the next trait. While effective if traits are positively correlated, this method may be limited by the complex evolutionary relationships among traits (Hazel 1943; Bernardo 2002; Sofi et al. 2022). In modern plant breeding, independent culling and selection indices are commonly used to improve multiple traits simultaneously (Bernardo 2002; Rana et al. 2019). Independent culling selects individuals that meet minimum thresholds for each trait (Raza et al. 2019; Batista et al. 2021; Bakhshi et al. 2023), but unfavorable trait correlations can lead to the loss of desirable genotypes (Yan and Kang 2002). Selection indices combine traits linearly or nonlinearly, weighted according to breeding objectives (Hazel 1943; Yan 2014; Sofi et al. 2022), yet subjectivity in trait weights and truncation points can influence selection decisions (Yan 2014; Sofi et al. 2022).

Genotype $\times$ trait (GT) biplot analysis provides a robust statistical tool for examining relationships among traits, evaluating genotypes for multiple traits, and identifying individuals excelling in specific traits (Stansluos et al. 2023). However, GT biplots alone cannot account for the combined effect of all traits on grain yield. The genotype by yield $\times$ trait (GYT) biplot was developed to overcome this limitation, enabling the simultaneous evaluation of multiple traits in combination with yield (Yan and Fréreau-Reid 2018). The GYT approach has been applied in several crops, including oat (Yan 2014; Akcura et al. 2018), rapeseed (Gholizadeh et al. 2023), maize (Habib et al. 2020; Mousavi

et al. 2021; Shojaei et al. 2022), common bean (Hoyos-villegas and Kelly 2016; Sofi et al. 2022), safflower (Koç 2021), snap bean (Rebecca et al. 2018; de Sant'Anna et al. 2020), oilseed rape (Bakhshi et al. 2023), soybean (Yan and Rajcan 2002), wheat (Kiss et al. 2020; Al-ashkar et al. 2022; Elfanah et al. 2023), and cotton (Peixoto et al. 2022).

Common bean breeders aim to develop cultivars that balance high grain yield with superior disease resistance and micronutrient concentrations. However, elevated resistance and micronutrient concentrations are beneficial; new cultivars must also maintain competitive yield to achieve adoption. The GYT method addresses this need by ranking genotypes based on multitrait performance combined with yield. The Average Tester Coordinate (ATC) graph of the GYT biplot measures overall superiority and identifies strengths and weaknesses of genotypes relative to ideotype traits (Yan 2024; Yue et al. 2022; Shojaei and Ansarifard 2023). Despite the demonstrated usefulness of GT and GYT approaches globally, their integration into multitrait and multitrait evaluation of Ethiopian common bean genotypes remains limited. This study employed GT and GYT biplot analyses to dissect trait associations and identify superior common bean genotypes that combine high yield, elevated Fe/Zn concentrations, and disease resistance, addressing a key need in the Ethiopian common bean breeding program.

2 | Materials and Methods

2.1 | Description of the Study Sites

Two field experiments were conducted at Melkassa and Negele Arsi during the Meher season in 2019/20. Melkassa is located 117 km east of Addis Ababa, Ethiopia. The study site was located at 8°30'N latitude, 39°21'E longitude, and at an elevation of 1550 m above sea level (Figure 1). The annual rainfall and mean annual minimum and maximum temperatures were 763 mm, 14.0°C, and 33.0°C, respectively. The site has an Andosol soil type. The site had high phosphorus, organic matter, cation exchange capacity (CEC), and zinc contents (Table 1). Negele Arsi

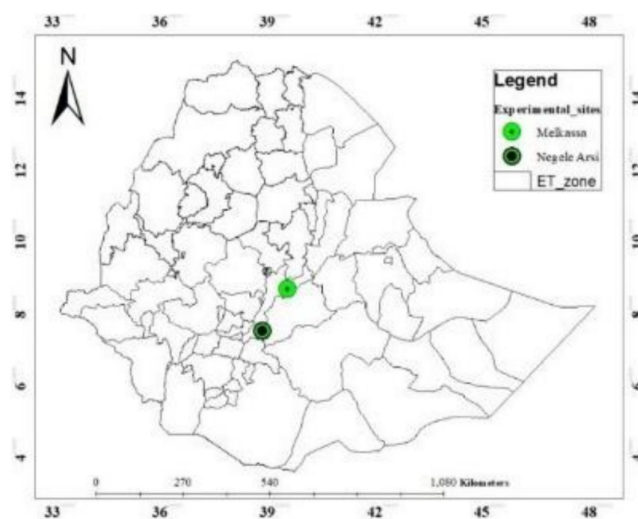


FIGURE 1 | The site map created using the geographic information system (ArcGIS) shows the testing locations, Melkassa and Negele Arsi, situated in Oromia Regional State.

TABLE 1 | Soil chemical and physical properties at two test locations.

Parameters	Abbreviation	Negele Arsi	Melkassa
Soil acidity	pH-H ₂ O	8.12	8.52
Organic matter	OC (%)	1.84	2.2
Total nitrogen	N (%)	0.14	0.16
Phosphorus	P (ppm)	7.98	20.99
Chloride	Cl (ppm)	32.52	15.02
Cation exchange capacity	CEC (Meq/100g)	30.11	31.61
Iron	Fe (ppm)	11.61	7.07
Manganese	Mn (ppm)	53.65	35.94
Copper	Cu (ppm)	1.38	1.28
Zinc	Zn (ppm)	2.18	2.38

is located 232.5 km south of Addis Ababa. The study site was located at 7°35'N latitude, 38°65'E longitude, and at an elevation of 1890 m above sea level (Figure 1). The study site mainly consisted of Nitisol soil. Moreover, this site contained high iron, manganese, copper, and chloride contents (Table 1). The annual rainfall and mean annual minimum and maximum temperatures were 807 mm, 13.8°C, and 23.3°C, respectively.

2.2 | Plant Materials and Field Experiments

In this study, 120 common bean genotypes were evaluated, comprising materials obtained from the International Center for Tropical Agriculture (CIAT) and the national breeding program, along with two standard checks (SER119 and SER125) (Table S1). The experiment was laid out in a randomized complete block design (RCBD) with a row-column arrangement and two replications. Seeds were sown at a spacing of 40 cm between rows, 1 m between plots and blocks, and 1.5 m between replications, with one seed per hill. At planting, 100 kg ha⁻¹ of NPS fertilizer was applied uniformly to each plot.

2.3 | Soil Sample Collection and Analyses

Prior to planting, soil samples were collected from the experimental plots at each test location. A soil auger was used to obtain samples from the 0–30 cm depth range, following a zigzag pattern. The collected soil samples were then mixed to form a composite sample. The samples were shade-dried before being passed through a 2-mm screen to determine the chemical composition of the soil. The soil pH was determined using a 2.5:1 solution of water and soil. A 0.5-M sodium bicarbonate solution (8.5 pH) was used as the extraction method for phosphorus from soil using the Olsen method (Olsen 1954). Similarly, the organic carbon content was determined using the Walkley–Black chromic acid wet oxidation method. The Kjeldahl method (Van Reeuwijk 2002) was used to measure the total nitrogen available

in the soil. The DTPA micronutrient extraction method was used to assess the availability of Fe and Zn (Lindsay et al. 1978). Available chlorides were extracted using ESISO 9297 (Chen et al. 2001). CEC was calculated using the ammonium acetate method.

2.4 | Iron and Zinc Sample Preparation and Quantification

Ten to fifteen well-developed pods were randomly selected from each plot at each sampling location. Prior to harvesting, pods were placed in clean envelopes. The hand-threshed pods were wiped with distilled water to remove soil contamination. The clean pods were carefully packed into clean paper bags. The samples were dried at 60°C for 60 h in paper bags (Stangoulis and Sison 2008). The samples were ground for 5 min in a Retsch Mixer Mill MM 400 equipped with ZrO grinding jars and balls (Retsch GmbH & Co. KG, Haan, Germany). After washing the jars with soap and distilled water, the surfaces were blotted dry using paper towels. The samples were analyzed using a Thermo Fisher Scientific ARL QUANT'X energy-dispersive X-ray fluorescence (EDXRF) model at CIAT, Kawanda, Uganda. Samples were prepared and analyzed using the procedures described in the user manual for ARL QUANT'X. Finally, the sample cups, which were carefully fitted with XRF films, were filled halfway and pressed slightly to level up and fill the cup bases. Before loading the samples into the machine, energy adjustment was performed using a standard copper sample to verify whether the parameter values of the final fine-gain setting met the specification of 25,000–30,000 and a peak FWHM (eV) between 150 and 170 eV. Ten samples per run were loaded at specified positions, and the amounts of Fe and Zn were determined by scanning each sample for 60 s. The sample cups were then spun to analyze all samples and record the intensities of the emitted X-rays. The results of the analysis were automatically displayed when all samples on the tray were measured. Standards with known Fe concentrations are routinely used for quality checks in the analysis of Fe and Zn.

2.5 | Data Collection

On the basis of the IPBGR (1982) descriptor of the common bean, data were collected to assess the quantitative traits. From five randomly selected and tagged plants, plant height (PH), number of pods per plant (PDPL), and number of seeds per pod (SDPD) were measured during the growing season. The plant height was measured from the base to the tip of each plant in the two middle rows. To determine the days to flowering (DF), we counted the number of days from planting until 50% of the plants in the two middle rows bloomed. The number of days to physiological maturity (DPM) in each plot was calculated when 90% of the plants had reached physiological maturity. To calculate the PDPL, five randomly selected plants in the middle two rows were counted as pods, and each plot was averaged. SDPD was determined by counting the seeds from five randomly selected pods per plot, and each plot was averaged. Hundred-seed weight (HSW) was measured using a random sample of 100 seeds from each plot. Grain yield (GY) was determined in grams per plot at a 12.5% moisture content. Finally, GY data were converted

to tons per hectare. Based on a disease recording scale of 1–9, common bean blight (CBBFL), halo blight (HBFL), and rust on leaves (RUSTFL) were recorded.

2.6 | Phenotypic Data Analysis

The Shapiro–Wilk test was performed on the residuals for each trait (Ghasemi and Zahediasl 2012). The p values for all measured traits except RUSTFL were greater than 0.05, indicating no significant departure from normality. Moreover, before the pooled analysis of variance, the field data from the two locations were assessed for homogeneity of error variances using Bartlett's test (Bartlett 1937) in R software version 4.5.1, and error variances across locations were homogeneous. The combined analysis of variance (ANOVA) was conducted using the lme4 version 1.1-37 (Bates et al. 2025) and lmerTest 3.1-3 (Kuznetsova et al. 2017) packages, where location and block were treated as random effects and genotypes as fixed effects.

2.6.1 | GT Biplot Analysis

Data were analyzed using the first two principal components derived from the singular value decomposition (SVD). Genotype*trait (GT) was generated using trait-standardized GT data with a scaling factor of 1 and a centering factor of 2. Furthermore, trait-focused single-value partitioning was employed, with an svp value of 2. For each genotype trait, a GT table was generated using mean values from the two locations (Table S2). GT displays the relationships between traits and genotypes in a biplot to show the strengths and weaknesses of traits and genotypes (Yan and Rajcan 2002). The which-won-where, discriminativeness versus representativeness, and ranking of genotypes were performed considering all traits of the GT biplot (Yan and Rajcan 2002) using the standardized values of days to flowering, days to physiological maturity, plant height, number of pods per plant, number of seeds per pod, hundred-seed weight, grain yield (ton/ha), iron, zinc, common bean blight, halo blight, and rust. The “metan” version 1.19.0 package was used to create the GT biplot graph.

2.6.2 | The GYT Table

The GYT analysis was performed following the steps described by (Yan and Fréreau-Reid 2018). First, the original genotype by trait (GT) two-way table (Table S4) was transformed into a GYT two-way table (Table S5). For traits such as PH, PDPL, SDPD, HSW, Fe, and Zn, the value of the grain yield*trait combinations were obtained by multiplying the grain yield value (GY) by the trait value for each genotype (e.g., GY*PH). A high grain yield*trait combination value was considered better for those traits. Conversely, for traits such as days to flower (DF), days to physiological maturity (DPM), common bean blight (CBBFL), halo blight (HBFL), and rust on leaves (RUSTFL), a smaller grain yield*trait combination value was preferred. Therefore, the grain yield*trait combination value was obtained by dividing the grain yield value by the trait value of each genotype. Second, standardize the raw GYT data table by each grain yield*trait combination to form a standardized GYT table, then

standardize the GYT table to a mean of zero and unit variance (Table S6). This process helps minimize bias due to differences in units among traits and allows for a more effective comparison of genotypes based on grain yield and other traits. This was done by centering (i.e., subtracting the mean) and dividing the centered value by the standard deviation within the respective grain yield*trait combinations using the following formula:

$$P_{ij} = \frac{T_{ji} - \bar{T}_j}{S_j}, \quad (1)$$

where P_{ij} is the standardized value of genotype i for grain yield*trait combination j in the standardized table, T_{ij} is the original value of genotype i for trait or yield*trait combination j in the GT or GYT table, $\bar{T}_j$ is the mean across genotypes for grain yield*trait combination j , and S_j is the standard deviation for grain yield*trait combination j .

Third, proper weights were applied to the yield-trait combinations according to their relative importance. Finally, the GYT index (superiority index) was calculated, which is the mean across weighted yield-trait combinations for each genotype. Lastly, the GYT index is computed by averaging the weighted yield-trait combinations for each genotype, providing a measure of overall superiority that can be used for genotype ranking.

Biplots were generated through the application of the Metan version 1.19.0 (Olivoto and Lúcio 2020) package in R software version 4.5.1, using the trait-specific standardized GYT tables (Table S6). The construction of these biplots involved singular value decomposition of the data, which had been standardized for each trait by scaling with the standard deviation and centering using tester-centered $G + E$ along with trait-focused symmetrical singular value partition.

2.6.3 | Correlation Analysis

Pearson's correlation analysis between traits and their correlation plot was performed using corrplot 0.92 (Wei and Simko 2021) and PerformanceAnalytics 2.0.8 (Peterson et al. 2024).

3 | Results

3.1 | Analysis of Variance, Mean Performance, and Correlation Between Traits

The combined ANOVA conducted across both sites demonstrated highly significant genotypic differences ($p < 0.001$) for all traits assessed (Table S3), highlighting substantial genetic variability among common bean genotypes. Location effects were also significant for most traits, except seeds per pod (SDPD) and Zn content, indicating a strong environmental influence. The interaction between genotype and environment was notable for certain traits, but not for days to maturity (DPM), plant height (PH), SDPD, and Fe, indicating consistent expression of these traits across locations. Replication effects were significant for grain yield (GY), days to flowering (DF), and halo blight disease (HBFL). Similarly, block effects had a significant impact on DPM, SDPD, GY, and HBFL, likely due to micro-environmental

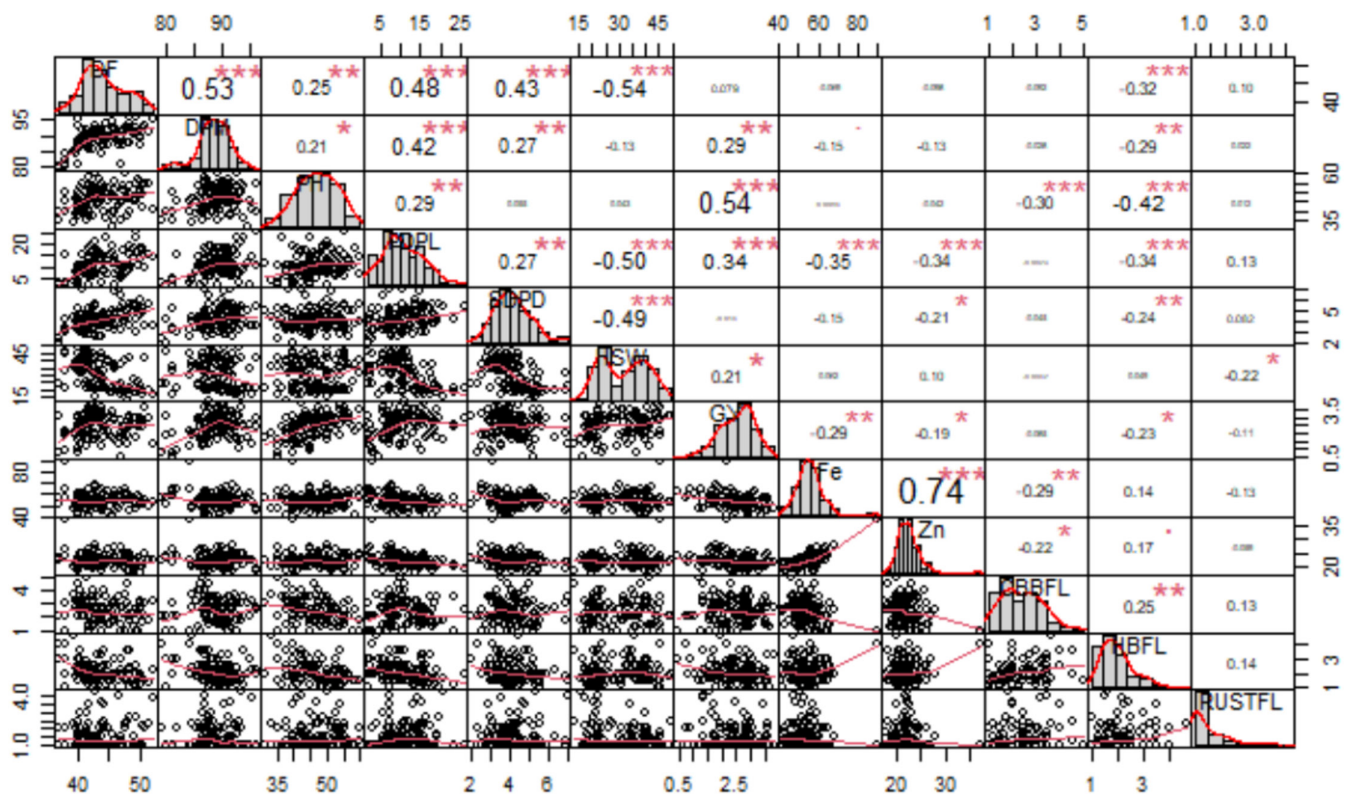


FIGURE 2 | Pearson's correlation coefficients among different quantitative traits of 120 common bean genotypes. DF, days to flowering; DPM, days to physiological maturity; PH, plant height; PDPL, pods per plant; SDPD, seeds per pod; HSW, hundred seed weight per plot (grams); GY, grain yield per hectare (ton); Fe, iron (ppm); Zn, zinc (ppm); CBBFL, common bean blight; HBFL, halo blight; RUSTFL, rust on leaves.

variations such as soil fertility differences within the sites (Table 1). The highest mean of GY ton ha^{-1} (3.81) was observed in G18 followed by G63 (3.70), G81 (3.62), G94 (3.62), and G19 (3.61), outperforming the check cultivars G99 and G100, which yielded 3.43 and 3.52 tons per hectare, respectively (Table S2). Genotype G49, on the other hand, gave the lowest grain yield (0.47 ton/ha). Mean Fe and Zn concentration over two locations and genotypes sampled was 54.31 and 22.12 ppm, with genotypic mean Fe and Zn concentration ranging from 41.4 to 89.4 ppm and 17.74 to 37.19 ppm, respectively (Table S2). The lowest iron and zinc levels were observed in genotypes G52 and G2, respectively. Significant positive and negative correlations between the assessed traits were observed in this study (Figure 2). Iron (Fe) showed a significant strong positive correlation ($r=0.74$) with zinc (Zn) content. The results also revealed a substantial positive correlation ($r=0.54$) between plant height (PH) and grain yield (GY). Moreover, DF was significantly correlated with the DPM ($r=0.53$), PDPL ($r=0.48$), and SDPD ($r=0.43$). On the other hand, hundred seed weight (HSW) was significantly negatively correlated with DF ($r=-0.54$), PDPL ($r=-0.50$), and SDPD ($r=-0.49$) (Figure 2).

3.2 | Genotype by Trait (GT) Biplot

The sum of the first two principal components (PC1 and PC2) explained 43.8% of the total variation, with PC1 and PC2 explaining 27.54% and 16.26%, respectively (Figure 3A). The relatively low explanatory power of GT may be attributed to several factors, including the substantial complexity of traits,

environmental influences, multicollinearity among traits, or the presence of non-linear relationships that principal component analysis fails to adequately capture (Atnaf et al. 2017; Welderufael and Abay 2023; Yan and Fréreau-Reid 2018).

3.2.1 | Traits Correlations and Profiles

As shown in the GT biplot, small angles indicate positive correlations between traits based on the trait-standardized data. However, the vectors forming the exact angles of 90° suggest no correlation. In contrast, diverging rays forming a large angle of approximately 180° indicate a negative correlation (Yan and Rajcan 2002; Sofi et al. 2022). Accordingly, GY was positively correlated with PH, DF, DPM, PDPL, and SDPD (Figure 3A). Similarly, significant positive correlations were found between iron (Fe), zinc (Zn), and hundred seed weight (HSW). In contrast, obtuse angles among PDPL, SDPD, and RUSTFL were negatively associated with Fe, Zn, and HSW, whereas HBFL and CBBFL angles were negatively correlated with GY and PH (Figure 3A). The low level of correlation between traits shown by the GT biplot was also confirmed by the values of the Pearson correlation among traits (Figure 2), because the GT biplot only captured 43.8% of the total variation and had low goodness of fit. In addition, the GT biplot adequately represented the total variation in PH, Fe, Zn, HSW, HBFL, PDPL, and CBBFL among the common bean genotypes. However, the vector lengths of the DPM, DF, GY, RUSTFL, and SDPD traits were comparatively short, suggesting that the GT biplot could not accurately represent these traits because of a lack of correlation between them.

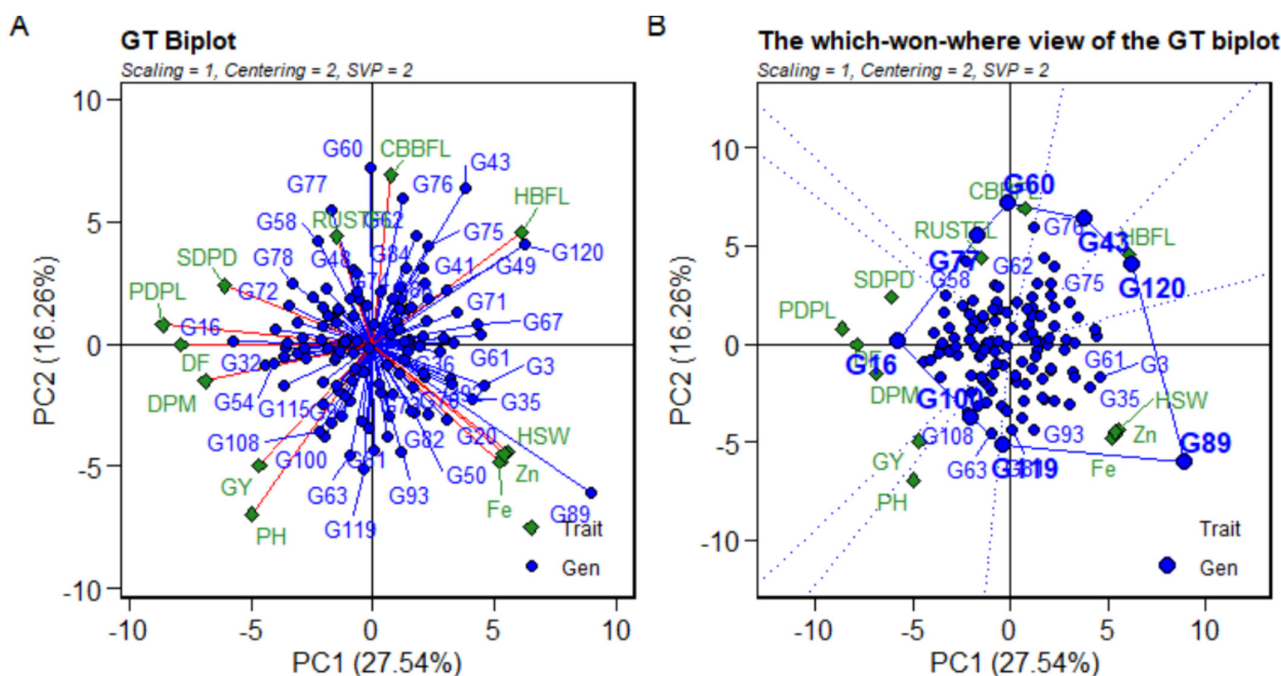


FIGURE 3 | (A) GT biplot of trait relationship of 118 common bean genotypes and two standard check cultivars. (B) A which-won-where biplot within a genotype by trait analysis. DF, days to flowering; DPM, days to physiological maturity; PH, plant height; PDPL, number of pods per plant; SDPD, number of seeds per pod; HSW, hundred seed weight per plot (grams); GY, grain yield per hectare (ton); Fe, iron (ppm), Zn, zinc (ppm); CBBFL, common bean blight; HBFL, halo blight on leaves; RUSTFL, rust on leaves.

In contrast, the GT biplot showed trait profiles of the common bean genotypes (Figure 3A), based on the goodness of fit of the biplot.

3.2.2 | Grouping of Genotypes Based on GT Biplot

The evaluated traits and genotypes were classified using “which-won-where” GT biplot data (Figure 3B). The polygonal view was formed by connecting the genotypes that were farthest away in all directions. A line drawn from the origin of the biplot intersects each side of the polygonal view to draw a perpendicular line. Genotypes at the vertex of each sector displayed the highest values for each trait. Accordingly, G89 was identified as a favorable allele source for HSW, Fe, and Zn, whereas G16 was the most favorable allele source for DF, DPM, SDPD, PDPL, and G100 for GY (Figure 3B). Notably, genotypes G16 and G89, positioned near the vertex, exhibited superiority for the majority of the measured traits (Figure 3B). Similar findings have been reported in earlier studies for various traits in common bean (Sofi et al. 2022), cotton (Peixoto et al. 2022), sorghum (Welderufael and Abay 2023), oat (Yan and Frégeau-Reid 2018), sunflower (Gholizadeh and Ghaffari 2023), and sesame (Boureima and Yaou 2019).

3.3 | GYT Analysis

Table S4, which contains GT data, serves as the basis for the generation of the GYT table data. Each column represents a combination of yield and other traits. To this end, traits with higher desirable values were multiplied by yield, whereas traits with lower favorable values were divided by yield. The GYT table data

were used to create a GYT biplot, which is a graphical representation. The first principal component of the GYT biplot accounted for 70.69% of the total variation, whereas the second principal component accounted for 9.67% of the total variation. Overall, the biplot explained 80.36% of the variation, which was significantly higher than that of the GT biplot. Consequently, a larger value is considered desirable in the GYT table (Figure 4). The findings align with previous research conducted by Welderufael and Abay (2023), Yan et al. (2019) and Faheem et al. (2023), who previously reported a higher proportion of the GYT total variation.

3.3.1 | Correlations Among Various Trait Combinations

Yan and Frégeau-Reid (2018) proposed a positive correlation when the angle between trait vectors was acute ($< 90^\circ$). In contrast, an obtuse angle ($> 90^\circ$) suggests a negative correlation. However, when the angle was 90° , there was no correlation between traits. The tester view of GYT biplot and correlation heatmap suggests the positive strong correlation among most of yield*trait combinations, with correlation coefficients ranging from 0.34 to 0.98 (Figure 5). This is a key feature of the GYT biplot compared to the GT biplot because of its ability to rank genotypes graphically and meaningfully based on yield trait combinations. The results demonstrated a strong positive association between GY/DPM and GY*Fe, GY*Zn, GY*PH, and GY/DF. Conversely, GY*Fe is strongly associated with GY*Zn and GY/DF. Furthermore, GY*Zn was strongly correlated with GY/DF and GY*PH. GY*PH was strongly correlated with GY/DF (Figure 5). Overall, the GYT biplot revealed positive associations among most trait combinations, confirming the possibility of selecting genotypes with

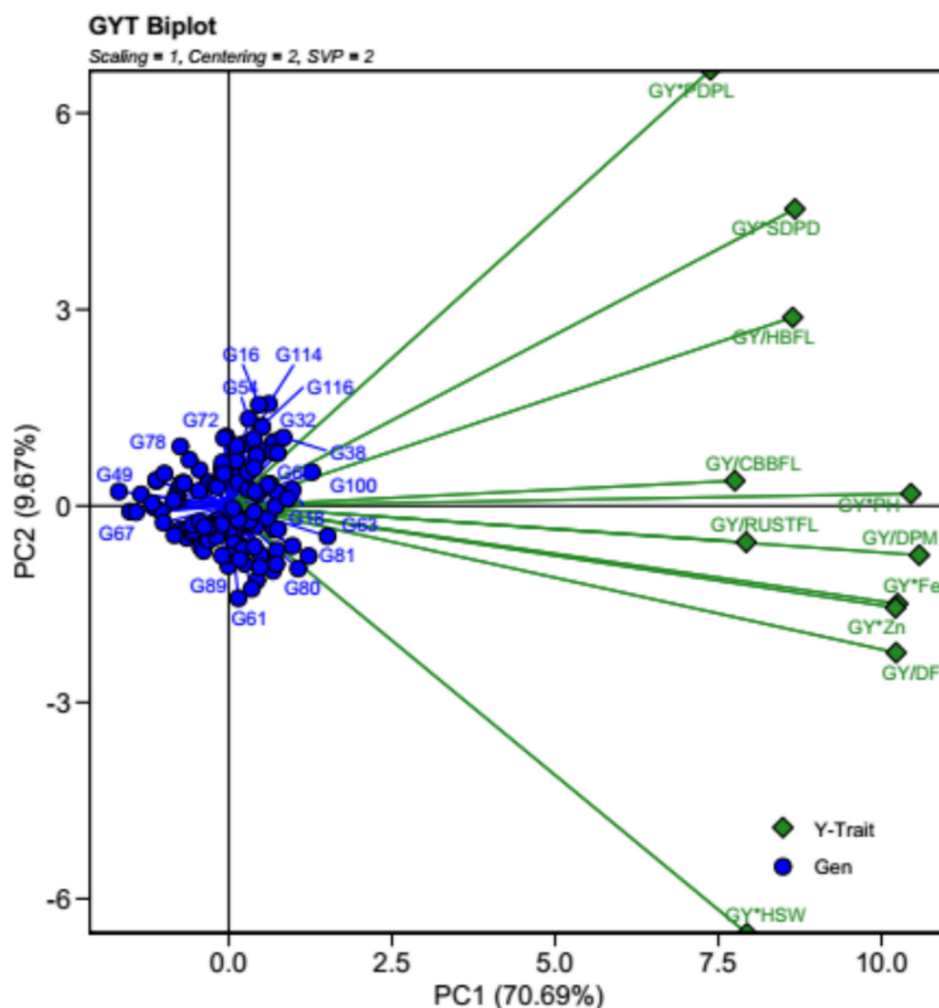


FIGURE 4 | The tester vector view of the GYT biplot shows associations between grain yield * trait combinations. GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, number of pods per plant; GY*SDPD, number of seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/ HBFL, halo blight on leaves; GY/RUSTFL, rust on leaves.

balanced trait performance. This observation is consistent with previous reports on wheat (Merrick et al. 2020; Faheem et al. 2023), mung bean (Karuniawan et al. 2025), and maize (Shojaei et al. 2024).

3.3.2 | Selection on the Basis of Multiple Trait Profile

The polygon of which-won-where separated the biplot into nine sectors, and the yield trait combinations were placed in three sectors. Genotypes G63, G81, and G80 present high values for GY*Fe, GY*Zn, GY*PH, GY*HSW, GY/DPM, GY/DF, GY/RUSTFL, and GY/CBBFL (Figure 6). Genotype G100 had high values for GY*SDPD and GY/ HBFL. In contrast, G114 had high values of GY*PDPL. In this way, G63, G80, G81, G100, and G114 genotypes exhibited superior performance for different sets of traits (Figure 6). In contrast, G49, G89, and G120 do not have association with any yield * trait combinations, indicating that these genotypes lacked the desired traits. Genotypes G63, G100, G81, G80, and G18 presented the highest mean values for the superiority index (Table 2). Among these genotypes, G63 and G80 had negative PDPL

values, indicating that these genotypes produce a high number of pods per plant. The yield * trait combinations positioned at the center of the concentric circles depicted in Figure 7, including GY/RUSTFL, GY/CBBFL, GY/ HBFL, PH * GY, DPM/ GY, and Fe * GY, demonstrated a high degree of representativeness. Furthermore, these central yield * trait combinations exhibited a balanced correlation with other yield * trait combinations. Therefore, GY/RUSTFL, GY/CBBFL, GY/ HBFL, PH * GY, DPM/ GY, and Fe * GY can be considered ideal yield * trait combinations.

3.4 | Superiority Rank of Genotypes

Figure 8 shows the ATC view of the GYT biplot generated from the standardized yield * trait combination data. The ATC view of the GYT biplot graphically illustrates the strengths and weaknesses of the genotypes, and ranks them based on their overall superiority. The small circle in the biplot indicates the average yield trait combinations, and the line passes through the biplot origin; the average yield * trait combination is called the average tester axis (ATA) and is used to rank genotypes based on

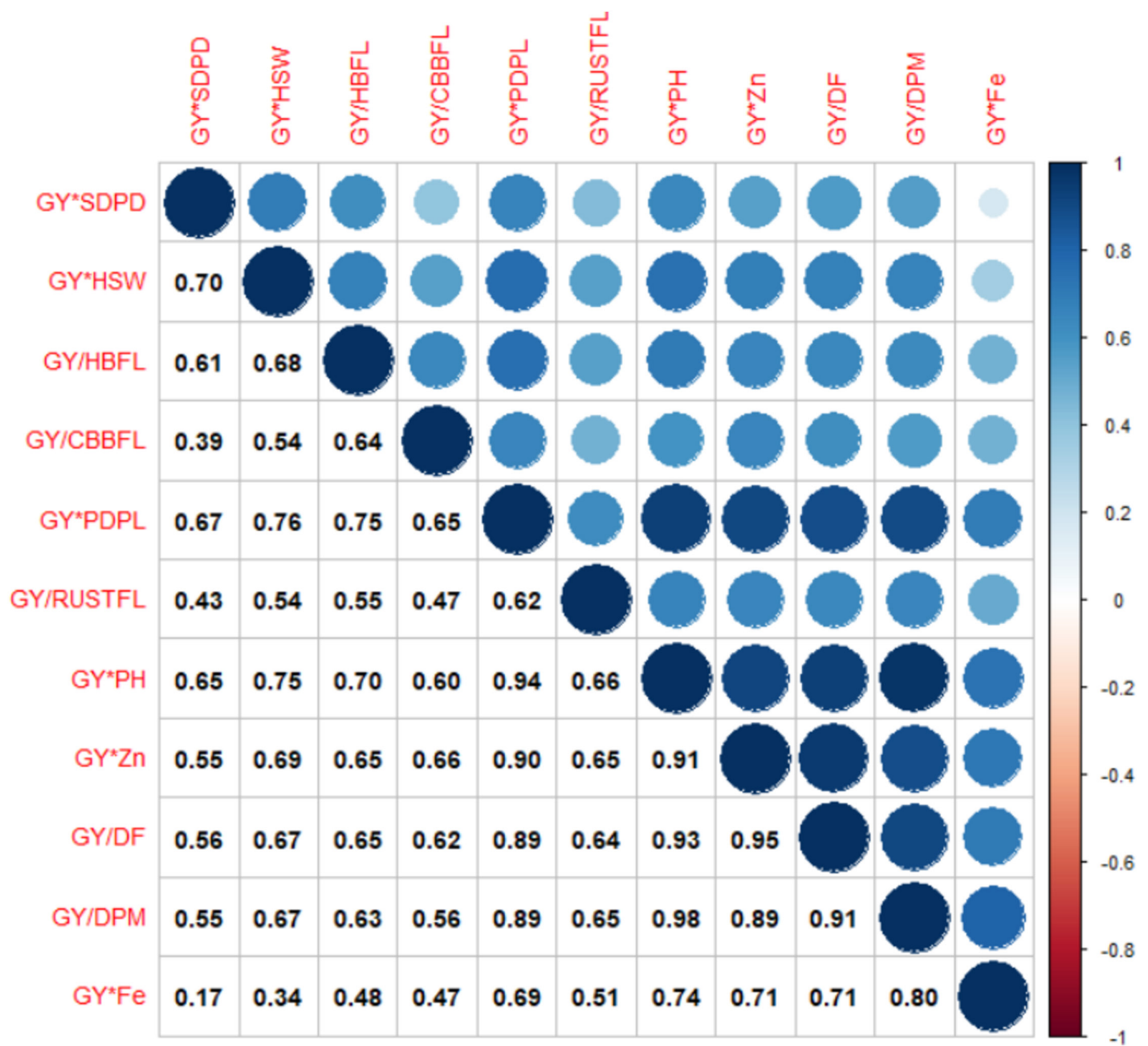


FIGURE 5 | Correlation heatmap of grain yield for all trait combinations of 120 common bean genotypes. GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, pods per plant; GY*SDPD, seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/HBFL, halo blight on leaves; GY/RUSTFL, rust on leaves.

their overall superiority. Genotypes located close to the ATA tend to have balanced trait profiles, whereas those located far from the ATA in either direction have apparent strengths and/or weaknesses. Ten most superior and five least superior common bean genotypes were identified using the overall superiority index of the grain yield*trait combinations (Table 2 and Table S6). Among these superior genotypes, G63, G100, G99, and G18, located in the center of the concentric circles, showed the best yield*trait combination profile. The genotypes G63, G100, G81, G80, and G18 were also ranked from most favorable to least favorable based on the superiority index, which considered all combinations of yield and traits (Table 2 and Table S6). Similar studies also reported in common bean (Sofi et al. 2022), sunflower (Gholizadeh and Ghaffari 2023), oat (Yan 2024), and sorghum (Welderufael and Abay 2023; Welderufael et al. 2024).

4 | Discussion

The combined ANOVA conducted across both sites demonstrated highly significant genotypic differences for all traits assessed, highlighting substantial genetic diversity among common bean genotypes. The top-performing genotypes for a particular trait could be valuable germplasm sources for further common bean breeding. Genotypes for Fe and Zn concentrations above the acceptable thresholds for Fe, ranging from 34 to 92 ppm (Beebe 2020) with a global average target of 50 ppm (Glahn and Noh 2021) and 21–59 ppm for Zn with a global target of 40 ppm (Philipo et al. 2021), may serve as promising candidates for biofortification of beans through breeding to achieve maximum levels of these micronutrients. The results revealed that genotypes G18, G63, G94, and G81 were promising for

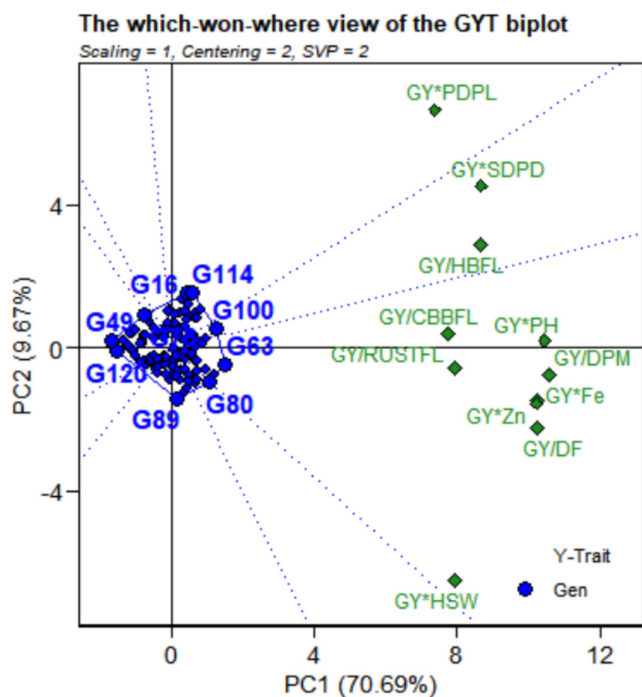


FIGURE 6 | “Which-won-where” view of the genotype by yield * trait (GYT) biplot of agronomic, disease, and micronutrient trait combinations of common bean genotype profiling. GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, pods per plant; GY*SDPD, seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/HBFL, halo blight on leaves; GY/RUSTFL, rust on leaves.

selection, as they exhibited elevated yields ranging from 0.47 to 3.81 GY/ha. The genotypes also showed considerable variation in micronutrient content, with Fe concentrations ranging from 41.4 to 89.4 ppm (mean 51.6 ppm) and Zn concentrations from 17.7 to 37.2 ppm (mean 24.5 ppm). This variation highlights the potential for simultaneous genetic improvement of both Fe and Zn through biofortification-oriented breeding. Analogous to the current finding, previous studies have observed a diverse range of yield values (Ambrósio et al. 2024), iron and zinc concentrations (Beebe 2020; Diaz et al. 2022; Ejigu et al. 2024) in common bean genotypes.

Simultaneous improvement in crop yield is a key objective, but breeding for specific traits can lead to trade-offs, where improving one trait may negatively impact another (Yan et al. 2019; Esposito et al. 2023; Derbyshire et al. 2024). To overcome these limitations, the present study employed both GT and GYT analyses to assess the performance of common bean genotypes. The GT biplot effectively shows distinct trait associations among common bean genotypes, offering a dual benefit. Specifically, it highlights G89 as a donor for high seed weight and elevated Fe/Zn concentrations, while genotypes G60, G43, and G120 are identified for their resistance to common bacterial blight and halo blight. However, these genotypes show lower yield potential and are therefore not ideal for direct release; they are valuable for exploiting genetic resources in parental selection and trait gene pyramiding in future crossing

programs. Yan and Frégeau-Reid (2018) demonstrated that the GT biplot effectively identifies genotypes in oat contributing specific quality traits from those excelling in yield. Similarly, Merrick et al. (2020) in wheat and Wolderufael et al. (2024) in sorghum used GT biplot to highlight trait-specific parents for disease resistance and biofortification.

In contrast, breeders can select superior genotypes using the GYT biplot, which considers their combined performance in yield and other desirable traits, a method that offers more insight than simpler index selection approaches, which can be more subjective (Yan and Frégeau-Reid 2018; Yan et al. 2019; Wolderufael and Abay 2023). In this way, genotypes with high yield and superior Fe/Zn concentrations were identified along with resistance to diseases. Genotypes G63, G100, G81, G80, and G18 showed a favorable combination of high yield, elevated levels of Fe/Zn in their grain, and resistance to diseases, making them promising parents or direct candidates for multilocation trials and variety release. Moreover, selection using the GYT index can minimize the risk of recommending low-yielding genotypes (Yan et al. 2019).

The GYT biplot showed strong positive correlations between most tested trait combinations, allowing breeders to identify superior genotypes by combining important traits with yield for simultaneous genetic improvements. Strong correlations between yield and other traits can be indicative of pleiotropism and genetic linkages, which would enable simultaneous improvements in both yield and other traits (Dilday et al. 1990). Furthermore, a strong positive correlation was observed between Fe and Zn. This implies that selection for increased iron content is also likely to lead to an increase in zinc content, which is advantageous for breeding programs targeting the simultaneous biofortification of beans with both minerals (Phuke et al. 2017). Previous studies have also reported a substantial positive correlation between Fe and Zn (Yan and Frégeau-Reid 2018; Wolderufael and Abay 2023), which is in agreement with the current study. Furthermore, positive correlations between yield resistance combinations suggest that resistance contributes to yield stability under field conditions. Comparable findings were documented in other crops (Merrick et al. 2020; Derbyshire et al. 2024), with the combination of disease resistance and yield as key indicators for stable cultivar performance.

Our study used GT and GYT analyses, providing valuable insights; however, certain limitations should be acknowledged. Specifically, the first two principal components account for 43.8% and 80.36% of the variation, indicating that some trait information is not fully captured in the biplots. The limited genotypic data from just two sites make it challenging to draw firm conclusions about genotypic performance across different environments. Additionally, GT and GYT biplots primarily function as descriptive tools, illustrating multiple-trait relationships and yield-trait combinations without possessing predictive capabilities. To achieve consistent genetic progress, it is essential to couple marker-assisted selection with cooking time assessments and conduct extensive multilocation, multiyear trials to further validate identified candidate genotypes. Recognizing these limitations is vital for highlighting the value and defining the scope of the present findings, as well as for setting clear

TABLE 2 | The top 10 high-performing and bottom five low-performing common bean genotypes were identified using the GYT index.

Genotype code	GY*PH	GY*PDPL	GY*SDPD	GY*HSW	GY*Fe	GY*Zn	GY/DF	GY/DPM	GY/CBBFL	GY/HBFL	GY/RUSTFL	Av.SI
Top 10 genotypes												
G63	1.97	-0.08	1.74	2.54	1.63	1.68	1.86	1.72	3.09	3.83	2.19	2.01
G100	2.26	1.36	2.62	0.97	1.81	1.94	1.54	1.55	1.45	1.65	1.12	1.66
G81	1.97	0.86	0.44	2.55	1.96	1.67	1.8	1.77	2.14	1.76	0.63	1.60
G80	1.89	-0.43	1.11	2.17	1.4	1.33	1.72	1.6	2.08	1.15	1.16	1.38
G18	1.09	2.09	1.03	0.3	1.31	1.89	1.92	1.91	0.37	-0.23	2.32	1.27
G94	1.97	0.53	0.66	2.07	1.87	2.34	0.93	1.44	0.06	1.76	-0.10	1.23
G99	1.31	0.83	2.16	0.95	1.35	1.17	1.47	1.34	-0.2	0.64	1.86	1.17
G38	1.07	1.68	0.78	-0.09	0.26	0.96	1.02	1.26	0.45	3.25	1.75	1.13
G82	1.25	1.28	0.03	1.13	1.49	1.47	1.15	0.87	0.63	0.08	1.43	0.98
G113	0.74	0.11	0.73	1.79	1.02	0.86	1.27	1.04	0.73	0.81	1.57	0.97
Bottom 5 genotypes												
G97	-1.62	-1.52	-1.28	-1.43	-1.80	-1.89	-1.78	-2.04	-1.10	-1.26	-1.00	-1.52
G71	-1.82	-0.87	-2.05	-1.63	-1.98	-2.07	-1.98	-2.13	-1.26	-1.64	-1.76	-1.74
G67	-2.01	-1.54	-2.10	-1.35	-2.25	-2.36	-2.19	-2.25	-1.33	-1.47	-1.33	-1.84
G120	-2.12	-1.57	-2.29	-1.65	-2.35	-2.32	-2.12	-2.25	-1.35	-1.80	-1.82	-1.97
G49	-2.38	-1.58	-2.11	-1.96	-2.73	-2.72	-2.79	-2.77	-1.21	-1.86	-1.73	-2.17

Note: Av.SI, average superiority index; GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, pods per plant; GY*SDPD, seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/HBFL, halo blight on leaves; GY/RUSTFL, rust on leave.

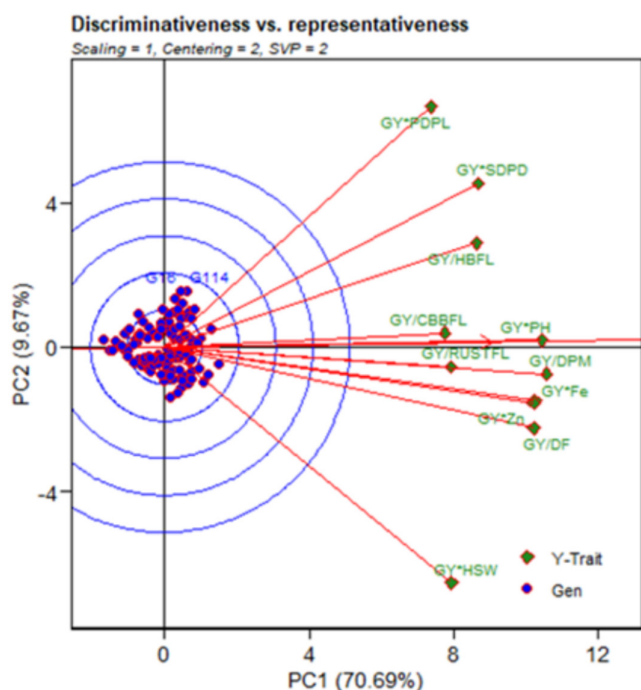


FIGURE 7 | Ranking trait biplot based on both discrimination and representativeness. GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, number of pods per plant; GY*SDPD, number of seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/HBFL, halo blight on leaves; GY/RUSTFL, rust on leaves.

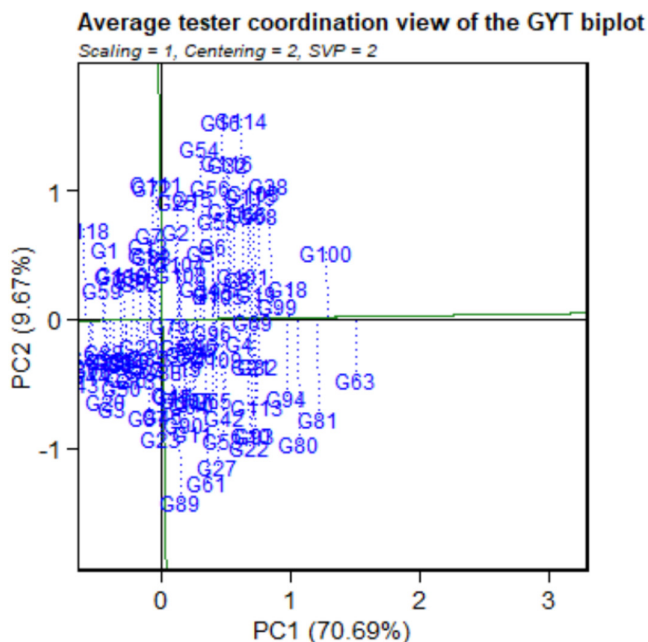


FIGURE 8 | The Average Tester Coordination (ATC) view of the genotype by yield×trait (GYT) biplot of 118 and two standard checks were evaluated at two locations. GY/DF, days to flowering; GY/DPM, days to physiological maturity; GY*PH, plant height; GY*PDPL, pods per plant; GY*SDPD, seeds per pod; GY*HSW, hundred seed weight per plot (g); GY, grain yield per hectare (ton); GY*Fe, iron (ppm); GY*Zn, zinc (ppm); GY/CBBFL, common bean blight; GY/HBFL, halo blight; GY/RUSTFL, rust on leaves.

directions for future variety release and breeding programs. In spite of these limitations, the results provide practical guidance for bean breeding strategies: crossing the promising candidate genotypes identified by the GYT index with G89 (a donor for high Fe and Zn content identified by the GT biplot), followed by further crossing with G60, G43, and G120 (donors for major disease resistance), would generate progenies that combine high yield, improved nutritional quality, and disease resistance. Such a strategic breeding approach not only meets the current variety release requirements but also supports long-term goals of trait accumulation and genetic gain. Collectively, these findings suggest that the combination of GYT with GT biplots is a validated and practical method, consistent with studies in legumes (Sofi et al. 2022; Karuniawan et al. 2025), cereals (Yan and Frégeau-Reid 2018; Faheem et al. 2023; Welderufael and Abay 2023; Welderufael et al. 2024), and oilseeds (Gholizadeh and Ghaffari 2023).

5 | Conclusions and Recommendations

Identifying and selecting high-performing common bean genotypes with desirable traits for yield, micronutrient concentrations, and disease resistance is a critical strategy for combating food insecurity and malnutrition in Ethiopia. In this study, GT and GYT analyses were employed to identify genotypes that combined high yield with superior Fe/Zn concentrations and disease resistance. The results reveal the practical value of integrating these methods into breeding programs, as they enable the identification of nutritionally superior, disease-resistant, and high-yielding genotypes suitable for variety release and parental selection. Particularly, the GYT biplot was more comprehensive than the GT biplot, as it ranked genotypes based on ideotypes and multiple traits simultaneously, thereby showing a clear assessment of both strengths and weaknesses. These two methods support breeders in selecting farmer-preferred varieties, designing new populations, and making informed decisions regarding cultivar release. Based on the GYT index, genotypes NABE14, SER125, RWR2154, RWR1873, and BFS10 were identified as superior, making them the best candidates for variety release and parental use. The development of these promising genotypes into successful varieties requires an integrated strategy. Future research should combine GYT and stability analyses across environments, while also prioritizing key consumer traits like cooking time. Augmented with marker-assisted selection, this strategy will ensure the accurate and efficient breeding of high-yielding, durable resistance, and elevated Fe/Zn concentrations beans that meet the demands of both farmers and consumers.

Acknowledgments

The authors appreciate the support obtained from the Addis Ababa University (AAU) Department of Microbial Sciences and Genetics throughout the fieldwork. The authors would also like to thank the Ethiopian Institute of Agricultural Research for funding support. The authors are grateful to the Melkassa Agricultural Research Center (MARC) and Negele Arsi Research staff for providing their experimental sites, equipment for the field trials, and unwavering assistance throughout the field trials.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Table S1:** Genotype code and names of tested common bean genotypes used in this study. **Table S2:** Average of measured traits for the two locations in 120 common bean genotypes in this study. **Table S3:** Combined analysis of variance (ANOVA) results of 11 traits for 120 common bean genotypes. **Table S4:** Genotype by yield*trait (GYT) data for 120 common bean genotypes. **Table S5:** Genotype by yield*trait (GYT) data for 120 common bean genotypes.

Table S6: Standardized genotype by yield*trait (GYT) data and superiority index (SI) for 120 common bean genotypes.